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GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT 3168  
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His  
1045 1050 1055

5 GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA 3216  
Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu  
1060 1065 1070

10 GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG 3264  
Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly  
1075 1080 1085

15 ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT 3312  
Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr  
1090 1095 1100

GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA 3360  
Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser  
1105 1110 1115 1120

GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT 3408  
Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys  
1125 1130 1135

25 GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT 3456  
Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr  
1140 1145 1150

30 GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT 3504  
Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile  
1155 1160 1165

35 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552  
Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu  
1170 1175 1180

40 CTC CTT ATG GAG GAA 3567  
Leu Leu Met Glu Glu  
1185

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser  
1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn  
                   20                  25                  30

5 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn  
                   35                  40                  45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp  
                   50                  55                  60

10 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu  
                   65                  70                  75                  80

15 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile  
                   85                  90                  95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala  
                   100                  105                  110

20 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg  
                   115                  120                  125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile  
                   130                  135                  140

25 Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr  
                   145                  150                  155                  160

30 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile  
                   165                  170                  175

Phe Gly Glu Ala Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr  
                   180                  185                  190

35 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn  
                   195                  200                  205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp  
                   210                  215                  220

40 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu  
                   225                  230                  235                  240

45 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile  
                   245                  250                  255

Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile  
                   260                  265                  270

50 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn  
                   275                  280                  285

Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu  
                   290                  295                  300

	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe	
	305					310					315					320	
5	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Gly	Asn	
					325					330					335		
	Ile	Thr	Ser	Pro	Ile	Tyr	Gly	Arg	Glu	Ala	Asn	Gln	Glu	Pro	Pro	Arg	
				340					345					350			
10	Ser	Phe	Thr	Phe	Asn	Gly	Pro	Val	Phe	Arg	Thr	Leu	Ser	Asn	Pro	Thr	
			355					360					365				
	Leu	Arg	Leu	Leu	Gln	Gln	Pro	Trp	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg	
15		370					375					380					
	Gly	Val	Glu	Gly	Val	Glu	Phe	Ser	Thr	Pro	Thr	Asn	Ser	Phe	Thr	Tyr	
	385					390					395					400	
20	Arg	Gly	Arg	Gly	Thr	Val	Asp	Ser	Leu	Thr	Glu	Leu	Pro	Pro	Glu	Asp	
					405					410					415		
	Asn	Ser	Val	Pro	Pro	Arg	Glu	Gly	Tyr	Ser	His	Arg	Leu	Cys	His	Ala	
				420					425					430			
25	Thr	Phe	Val	Gln	Arg	Ser	Gly	Thr	Pro	Phe	Leu	Thr	Thr	Gly	Val	Val	
			435					440					445				
	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr	Ile	Asp	Pro	
		450					455					460					
	Glu	Arg	Ile	Asn	Gln	Ile	Pro	Leu	Val	Lys	Gly	Phe	Arg	Val	Trp	Gly	
	465					470				475						480	
35	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	
					485				490						495		
	Arg	Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	Gln	Val	Asn	Ile	Asn	
			500					505						510			
40	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	Arg	Tyr	Ala	Ser	Ser	
			515					520					525				
	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val	
45		530					535				540						
	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	Lys	Thr	Met	Glu	Ile	
	545					550					555					560	
50	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	Thr	Asp	Phe	Ser	Asn	
					565				570					575			
	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly	Ile	Ser	Glu	Gln	
				580				585					590				